



## SEQUENCE LISTING

<110> Reinherz, Ellis L.  
 Freund, Christian  
 Li, Jing  
 Nishizawa, Kazuhisa  
 Wagner, Gerhard

<120> Cloning and Characterization of a CD2  
 Binding Protein (CD2BP2)

<130> 1062.1021-004

<140> 09/873,106

<141> 2001-06-01

<150> US 60/111,007

<151> 1998-12-04

<150> US 60/115,647

<151> 1999-01-13

<150> PCT/US99/26993

<151> 1999-11-15

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)...(1143)

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atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat 168
Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
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gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct 216
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      20              25              30

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ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264
Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
      35              40              45

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agc gat gag gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac	312
Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp	
50 55 60	
atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc	360
Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro	
65 70 75 80	
agc gag ggg ggt ggt cgg atc aca ccc ttt aac ctg cag gag gag atg	408
Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met	
85 90 95	
gag gaa ggc cac ttt gat gcc gat ggc aac tac ttc ctg aac cgg gat	456
Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp	
100 105 110	
gct cag atc cga gac agc tgg ctg gac aac att gac tgg gtg aag atc	504
Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile	
115 120 125	
cgg gag cgg cca cct ggc cag cgc cag gcc tca gac tcg gag gag gag	552
Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu	
130 135 140	
gac agc ttg ggc cag acc tca atg agt gcc caa gcc ctc ttg gag gga	600
Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly	
145 150 155 160	
ctt ttg gag ctc cta ttg cct aga gag aca gtg gct ggg gca ctg agg	648
Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg	
165 170 175	
cgt ctg ggg gcc cga gga gga ggc aaa ggg aga aag ggg cct ggg caa	696
Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln	
180 185 190	
ccc agt tcc cct cag cgc ctg gac cgg ctc tcc ggg ttg gcc gac cag	744
Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln	
195 200 205	
atg gtg gcc cgg ggc aac ctt ggt gtg tac cag gaa aca agg gaa cgg	792
Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg	
210 215 220	
ttg gct atg cgt ctg aag ggt ttg ggg tgt cag acc cta gga ccc cac	840
Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His	
225 230 235 240	
aat ccc aca ccc cca ccc tcc ctg gac atg ttc gct gag gag ttg gcg	888
Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala	
245 250 255	
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<210> 2
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<212> PRT
<213> Homo sapiens
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			20					25					30			
Gly	Ser	Gly	Gly	Pro	Gly	Ser	Arg	Phe	Lys	Gly	Lys	His	Ser	Leu	Asp	
		35					40					45				
Ser	Asp	Glu	Glu	Glu	Asp	Asp	Asp	Asp	Gly	Gly	Ser	Ser	Lys	Tyr	Asp	
	50					55					60					
Ile	Leu	Ala	Ser	Glu	Asp	Val	Glu	Gly	Gln	Glu	Ala	Ala	Thr	Leu	Pro	
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Ser	Glu	Gly	Gly	Gly	Arg	Ile	Thr	Pro	Phe	Asn	Leu	Gln	Glu	Glu	Met	
				85					90					95		
Glu	Glu	Gly	His	Phe	Asp	Ala	Asp	Gly	Asn	Tyr	Phe	Leu	Asn	Arg	Asp	
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Ala	Gln	Ile	Arg	Asp	Ser	Trp	Leu	Asp	Asn	Ile	Asp	Trp	Val	Lys	Ile	
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Asp	Ser	Leu	Gly	Gln	Thr	Ser	Met	Ser	Ala	Gln	Ala	Leu	Leu	Glu	Gly	
145					150					155				160		
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				165					170					175		
Arg	Leu	Gly	Ala	Arg	Gly	Gly	Gly	Lys	Gly	Arg	Lys	Gly	Pro	Gly	Gln	
			180					185					190			
Pro	Ser	Ser	Pro	Gln	Arg	Leu	Asp	Arg	Leu	Ser	Gly	Leu	Ala	Asp	Gln	
	195						200					205				
Met	Val	Ala	Arg	Gly	Asn	Leu	Gly	Val	Tyr	Gln	Glu	Thr	Arg	Glu	Arg	
	210					215						220				

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Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His  
 225 230 235 240  
 Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala  
 245 250 255  
 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu  
 260 265 270  
 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu  
 275 280 285  
 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met  
 290 295 300  
 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg  
 305 310 315 320  
 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp  
 325 330 335  
 Phe Asp Leu Tyr Thr  
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<210> 3  
 <211> 26  
 <212> PRT  
 <213> Homo sapiens

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 Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly  
 20 25

<210> 4  
 <211> 27  
 <212> PRT  
 <213> Caenorhabditis elegans

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 Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu  
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<210> 5  
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 20 25

<210> 6  
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 <212> PRT

<213> *Caenorhabditis elegans*

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Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu  
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<210> 7

<211> 29

<212> PRT

<213> *Saccharomyces cerevisiae*

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Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser  
1 5 10 15  
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20 25

<210> 8

<211> 27

<212> PRT

<213> *Saccharomyces cerevisiae*

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<210> 9

<211> 17

<212> PRT

<213> Artificial Sequence

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<223> Motif in CD2 binding region of CD2BP2

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<222> 1,2,4,5,6,7,9,10,11,12,13,14,15

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 3

<223> Xaa can be Tyr or Phe

<221> VARIANT

<222> 8

<223> Xaa can be Met or Val

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&lt;400&gt; 9

Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Tyr  
 1 5 10 15  
 Phe

&lt;210&gt; 10

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; CD2BP2 binding region

&lt;400&gt; 10

Pro Pro Pro Gly His Arg  
 1 5

&lt;210&gt; 11

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 11

Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro  
 1 5 10 15  
 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro  
 20 25 30  
 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro  
 35 40 45  
 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser  
 50 55 60  
 Leu Ser Pro Ser Ser Asn  
 65 70

&lt;210&gt; 12

&lt;211&gt; 8

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Kozak consensus sequence

&lt;400&gt; 12

ccgccacc

8

&lt;210&gt; 13

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Flag Epitope

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24

<210> 14  
<211> 8  
<212> PRT  
<213> Artificial Sequence

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<210> 15  
<211> 31  
<212> PRT  
<213> Gallus gallus

<220>  
<223> Flag Epitope

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<210> 16  
<211> 38  
<212> PRT  
<213> Drosophila melanogaster

<220>  
<223> Flag Epitope

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Arg Tyr Phe Lys Asn Gly  
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<210> 17  
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<212> PRT  
<213> Leishmania major

<220>  
<223> Flag Epitope

&lt;400&gt; 17

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			20					25					30		
Lys	Lys														

&lt;210&gt; 18

&lt;211&gt; 36

&lt;212&gt; PRT

<213> *Caenorhabditis elegans*

&lt;220&gt;

&lt;223&gt; Flag Epitope

&lt;400&gt; 18

Val	Ile	Asp	Thr	Lys	Trp	His	Tyr	Leu	Gly	Pro	Asp	Ser	Glu	Lys	Tyr
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			20					25					30		
Phe	Asn	Asp	Gly												
			35												

&lt;210&gt; 19

&lt;211&gt; 35

&lt;212&gt; PRT

<213> *Caenorhabditis elegans*

&lt;220&gt;

&lt;223&gt; Flag Epitope

&lt;400&gt; 19

Val	Glu	Ser	Ser	Trp	Arg	Tyr	Ile	Asp	Thr	Gln	Gly	Gln	Ile	His	Gly
1				5					10					15	
Pro	Phe	Thr	Ile	Gln	Met	Met	Ser	Gln	Trp	Tyr	Ile	Gly	Gly	Tyr	Phe
			20					25					30		
Ala	Ser	Thr													
			35												

&lt;210&gt; 20

&lt;211&gt; 35

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;223&gt; Flag Epitope

&lt;400&gt; 20

Ile	Glu	Ser	Gln	Trp	Lys	Tyr	Ile	Asp	Ser	Asn	Gly	Asn	Ile	Gln	Gly
1				5					10					15	
Pro	Phe	Gly	Thr	Asn	Asn	Met	Ser	Gln	Trp	Tyr	Gln	Gly	Gly	Tyr	Phe
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Thr Pro Thr  
35

<210> 21  
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<212> PRT  
<213> Saccharomces pombe

<220>  
<223> Flag Epitope

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<210> 22  
<211> 21  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Flag Epitope

<400> 22  
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1 5 10 15  
Pro Pro Gly His Arg  
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<210> 23  
<211> 62  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Flag Epitope

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35 40 45  
Gln Phe Tyr Asn Ser Lys Arg Ile Asp Phe Asp Leu Tyr Thr  
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<210> 24  
<211> 31  
<212> PRT  
<213> Homo sapiens

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&lt;220&gt;

&lt;223&gt; Flag Epitope

&lt;400&gt; 24

Trp	Tyr	Tyr	Lys	Asp	Pro	Gln	Gly	Glu	Ile	Gln	Gly	Pro	Phe	Asn	Asn
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Gln	Glu	Met	Ala	Glu	Trp	Phe	Gln	Ala	Gly	Tyr	Phe	Thr	Met	Ser	
			20					25					30		

&lt;210&gt; 25

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; Flag Epitope

&lt;400&gt; 25

Gln	Trp	Phe	Ser	Arg	Ser	Leu	Ala	Pro	Cys	Pro	Gly	Pro	Phe	Thr	Thr
1				5					10					15	
Gln	Glu	Met	Ala	Glu	Trp	Phe	Gln	Ala	Gly	Tyr	Phe	Ser	Met	Ser	
			20					25					30		

# NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: Sequences which lack a SEQ ID NO: tag are disclosed on pages 16, 19 and 20 of the specification. See attached Office Action

**Applicant Must Provide:** ONLY IF THE CRF DOES NOT CONTAIN SAID SEQUENCE.

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

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